SCHREIBER
Serial No. **Unknown**
U.S. National Phase of PCT/EP99/09759

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS

3. (Amended) Protein vaccine according to claim 1 [or 2], characterized in that it comprises a mixture of GP120 proteins of HIV which in each case differ from each other in their amino acid sequence in the region of the V2 loop and/or of the V3 loop.

6. (Amended) DNA vaccine according to claim 4 [or 5], characterized in that the mixture contains $\geq 10^3$ and preferably $\geq 10^4$ DNA molecules which differ from each other in their nucleic acid sequence.

7. (Amended) DNA vaccine according to [one of claims 4 to 6] claim 4, characterized in that it codes for a mixture of structurally different GP120 proteins of HIV, in which the vaccine contains a mixture of DNA molecules, the nucleic acid sequences of which differ from each other in the region coding for the V2 loop and/or in the region coding for the V3 loop.

11. (Amended) Nucleic acid sequence according to claim 9 [or 10], characterized in that the sequence is modified by the introduction of silent mutations.

12. (Amended) Nucleic acid sequence according to [claims 9 to 11]claim 9, characterized in that it contains the sequence given in SEQ ID NO: 9.

17. (Amended) Nucleic acid sequence according to claim 15 or [16] a single-stranded nucleic acid sequence which contains the region coding for the V2 loop and/or the region of GP120 coding for the V3 loop, characterized in that in the V3 loop a 247 bp-long Bg1II-XbaI fragment or a 283 bp-long Bg1II-NheI fragment is exchanged for a modified fragment, and in the V2 loop a 139 bp-long PstI-Bc1I fragment or a 339 bp-

long PstI-EcoRI fragment is exchanged for a modified fragment, the fragment/the fragments in each case containing inosine, a nucleic acid exchange or a mutation at at least 6 positions, the nucleic acid sequence being complementary to a nucleic acid sequence characterized in that it contains the sequence given in SEQ ID NO: 12 , characterized in that the fragment/the fragments contain(s) inosine, a nucleic acid exchange or a mutation at 9 to 20 positions.

18. (Amended) Double-stranded DNA which comprises hybrids of the single-stranded nucleic acid sequence according to claim 15 [or 17] with [the] a single-stranded nucleic acid sequence [according to claim 16 or 17] which contains the region coding for the V2 loop and/or the region of GP120 coding for the V3 loop, characterized in that in the V3 loop a 247 bp-long Bg1II-XbaI fragment or a 283 bp-long Bg1II-NheI fragment is exchanged for a modified fragment, and in the V2 loop a 139 bp-long PstI-Bc1I fragment or a 339 bp-long PstI-EcoRI fragment is exchanged for a modified fragment, the fragment/the fragments in each case containing inosine, a nucleic acid exchange or a mutation at at least 6 positions, the nucleic acid sequence being complementary to a nucleic acid sequence characterized in that it contains the sequence given in SEQ ID NO: 12.

27. (Amended) Expression vector, characterized in that it contains an inserted nucleic acid sequence according to [claims 9 to 14]claim 9.

33. (Amended) Vector mixture according to [one of claims 30 to 32]claim 30, characterized in that the plasmids can be expressed in *E. coli* as host cell.

34. (Amended) Vector mixture according to [one of claims 30 to 32]claim 30, characterized in that the plasmids can be expressed in eukaryotic cells, preferably in Cos, CHO or BHK cells, as host cells.

40. (Amended) Process according to claim 38 [or 39], characterized in that the nucleic acid sequence coding for a viral protein is the sequence according SEQ ID NO: 1 or SEQ ID NO: 11 or a fragment of same.

41. (Amended) Process for the preparation of the vector mixture according to [claims 33 and 34]claim 33, characterized in that plasmids, the nucleic acid sequences of which in each case differ from each other in the region coding for the V2 loop and/or in the region coding for the V3 loop in each case through random distribution of the bases at the varied nucleotide positions, are ligated into a vector which can be expressed in host cells.

43. (Amended) Process for the preparation of the host cells [according to claim 35 or 36, characterized in that the host cells are transformed] composing transforming *E.coli*. with a vector mixture according to [claims] claim 30 [to 32].

44. (Amended) Process for the preparation of a protein vaccine which comprises a mixture of viral protein molecules, characterized in that the molecules are sequence variants of a single viral protein or of part of same, the mixture containing $\geq 10^2$ sequence variants, which is obtainable by expression of a plasmid-DNA mixture which, because of the variation of nucleotide positions, contains randomly distributed sequence combinations [according to one of claims 1 to 3, characterized in that the host cells are cultivated] , said process comprising cultivating host cells according to [one of claims 35 to 37] claim 35 under conditions which allow the expression of the mixture of viral protein sequence variants.

45. (Amended) Process for the preparation of a DNA vaccine which codes for a mixture of structurally different virus proteins, characterized in that the vaccine contains a mixture of sequence variants of a viral DNA molecule or of part of same, the mixture containing $\geq 10^2$ DNA molecules which differ from each other in their nucleic acid sequence, where the mixture, because of the variation of nucleotide positions, contains

randomly distributed sequence combinations wherein said [according to [one of claims 4 to 8, characterized in that the] process is carried out according to claim 41 [or 42], wherein the plasmids [according to the invention being] are ligated into a vector which can be expressed in host cells of the organism to be vaccinated.

46. (Amended) A method of preparing a vaccine comprising forming a [Use of a] mixture of structurally different viral proteins which are sequence variants of a viral protein or of part of same, for [the preparation of a vaccine for] the prevention and/or therapy of a virus infection in humans.

47. (Amended) A method of preparing a vaccine comprising forming a mixture [Use of a protein mixture] according to [one of claims 23 to 25]claim 23 [for the preparation of a vaccine] for the prevention and/or therapy of a HIV infection in humans.

48. (Amended) A method of preparing a vaccine comprising forming [Use of] a mixture of DNA molecules which code for sequence variants of a viral protein or of part of same, for [the preparation of a vaccine for] the prevention and/or therapy of a virus infection in humans.

49. (Amended) A method of preparing a vaccine comprising [Use of] forming a nucleic acid mixture according to [claims 19 to 22]claim 19 for the [preparation of a vaccine for the] prevention and/or therapy of a virus infection in humans.

50. (Amended) A method of preparing a vaccine comprising [Use of] forming the nucleic acid mixture according to [one of claims 19 to 22]claim 19 for the [preparation of a vector mixture according to one of claims 30 to 32 which can be expressed] expression in host cells[, the host cells being] selected from the group consisting of *E. coli*, Cos, CHO and BHK cells.

51. (Amended) A method of producing a protein mixture which comprises sequence variants of the GP120 protein, characterized in that it is a mixture of proteins

which contain amino acid sequences which in each case differ from each other in the V2 loop and/or in the V3 loop, the mixture being obtainable by expression of a plasmid DNA mixture which, because of the variation of nucleotide positions, contains randomly distributed sequence combinations; said method comprising [Use of the vector mixture according to one of claims 30 to 32] expressing a vector mixture which contains a mixture of plasmids which contains an inserted double-stranded DNA which comprises hybrids of the single-stranded nucleic acid sequence according to claim 15 with a single-stranded nucleic acid sequence which contains the region coding for the V2 loop and/or the region of GP120 coding for the V3 loop, characterized in that in the V3 loop a 247 bp-long Bg1II-XbaI fragment or a 283 bp-long Bg1II-NheI fragment is exchanged for a modified fragment, and in the V2 loop a 139 bp-long PstI-Bc1I fragment or a 339 bp-long PstI-EcoRI fragment is exchanged for a modified fragment, the fragment/the fragments in each case containing inosine, a nucleic acid exchange or a mutation at at least 6 positions, the nucleic acid sequence being complementary to a nucleic acid sequence characterized in that it contains the sequence given in SEQ ID NO: 12; characterized in that the nucleic acid sequences of the plasmids differ in each case from each other in the region coding for the V2 loop and/or in the region coding for the V3 loop, where the mixture of the plasmids, because of the variation of nucleotide positions, contains randomly distributed sequence combinations [for the expression of a protein mixture according to one of claims 23 to 25].

52. (Amended) A method of preparing a protein mixture which comprises sequence variants of the GP120 protein, characterized in that it is a mixture of proteins which contain amino acid sequences which in each case differ from each other in the V2 loop and/or in the V3 loop, the mixture being obtainable by expression of a plasmid DNA mixture which, because of the variation of nucleotide positions, contains randomly distributed sequence combinations, said method comprising culturing a [Use of the] host cell according to [one of claims 35 to 37]claim 35 [for the preparation of a protein mixture according to one of claims 23 to 25].

54. (Amended) Pharmaceutical composition for the prevention and/or therapy of a virus infection, characterized in that it comprises a protein mixture and a nucleic acid mixture, the protein mixture comprising sequence variants of a viral protein or of part of same, and the nucleic acid mixture comprising DNA molecules which code for sequence variants of a viral protein or of part of same, said composition comprising [according to claim 53, characterized in that it comprises] a protein mixture according to claim 23 [claims 23 to 25] and a nucleic acid mixture which comprises double-stranded DNAs, the nucleic acid sequences of which are derived from the *env* sequence in SEQ ID NO: 1 or SEQ ID NO: 11 or a fragment of same, characterized in that the nucleic acid sequences in each case differ from each other in the region coding for the V2 loop and/or in the region coding for the V3 loop [according to claims 19 to 22].